**Toolkit Data Submission Instructions**

**For each submission, please submit the following information to** [**scge@mcw.edu**](mailto:scge@mcw.edu)**:**

**Part A) project information and tier access**

**Part B) completed metadata file**

**Part C) data (spreadsheets, images, SOP, etc.)**

**Part A:**

* PI/MPI name(s): Shengdar Q. Tsai
* POC name: Shengdar Q. Tsai
* Project Title: A novel T cell platform to define biological adverse effects of genome editing
* Initiative: check one:

Animal Reporter and Testing Centers

Biological Effects

Delivery Systems

Genome Editors

* Access: check one:

Tier 1 (your project team, DCC Toolkit team, NIH PO/PTL/SO)

Tier 2 (your project team, DCC Toolkit team, NIH PO/PTL/SO, + collaborating SCGE-funded team)

If Tier 2 – identify collaborating SCGE-funded project to be given access to data:

PI/MPI name and project:

All members of the collaborating SCGE-funded project team will be given access to the data unless a specific subset of the additional SCGE-funded project team is identified.

Tier 3 (internal access to entire SCGE consortium)

Tier 4 (external release to scientific community and public)

**Part B**

* We are providing a metadata file for data being submitted to the Toolkit. Metadata describes your experimental setup and is distinct from experimental data. Please see the “read me” tab for instructions and fill in as many fields as you can. Attach completed metadata file to email. The metadata will assist the Toolkit in making the data accessible, searchable, and assessable.
  1. Large lists of things such as primer sequences can be provided as a separate spreadsheet.

**Part C**

* Attach data files to email: xls, xlsx, csv, txt, jpeg, special format (let DCC know)
  1. For large files (e.g. sequence) or large number of files (e.g. images), please contact the Toolkit team at [scge@mcw.edu](mailto:scge@mcw.edu) prior to submission.

* 1. We are unable to extract data from graphs (bar or line graphs) so that data submitted needs to be in a spreadsheet format. Data can be raw values or number of replicates with calculated averages and errors.
  2. For the data files, please include information that describes each column and row (what is being measure, units of measure, etc.). Data labels should unequivocally tie to information in metadata files.
  3. Protocols can be submitted as PDF documents. Include lab information (individual who wrote the protocol) and whether the protocol can be included in the Toolkit.
  4. Submission of representative images files should include a description that includes the information necessary to identify and distinguish image files from one another (can be provided as a spreadsheet with all image file names included along with description). This might include tissue, gender, age, dose, treatment, staining, magnification, etc. The Toolkit intends to house representative images and is not intended to be an image repository.
* Successful data submission will be confirmed by the DCC through communication to the following group of people: PI/MPI, POC, NIH PO & SO, Colin Fletcher, and Deanna Portero
* Ideally within the two weeks following data submission, the DCC will schedule a Toolkit meeting with the POC to discuss in detail the submitted data and the metadata file.

Data submission will transition to a web submission process through <https://scge.mcw.edu/> in the near future. For the first round of data submission, please send the above information to [scge@mcw.edu](mailto:scge@mcw.edu). Questions regarding data submission can be directed to [scge@mcw.edu](mailto:scge@mcw.edu) or [mrdwinel@mcw.edu](mailto:mrdwinel@mcw.edu).